



crt sequences.ST25  
SEQUENCE LISTING

<110> St. Boniface General Hospital Research Centre  
Mesaeli, Nasrin  
<120> Transgenic Mouse over-expressing calreticulin (CRT) in vascular  
smooth muscle cells  
<130> 81190-2602  
<150> US 60/455399  
<151> 2003-03-18  
<160> 24  
<170> PatentIn version 3.2  
<210> 1  
<211> 2655  
<212> DNA  
<213> Artificial  
<220>  
<223> artificial construct of sm22a promoter and CRT cDNA

<220>  
<221> CDS  
<222> (1319)..(2653)  
<223> CRT coding sequence

<400> 1  
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tcctgggtga gactgaccct gcctgagggg tctctccttc cctctctcta ctcccttcct 180  
ccctctccct ctccctctct ctgtttcctg aggtttccag gattggggat gggactcaga 240  
gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca 300  
cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac 360  
tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg 420  
tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggg 480  
aggatctttc acgataagga ctattttgaa gggagggagg gtgacactgt cctagtcctc 540  
ttaccctagt gtcctccagc cttgccaggc cttaaaccatc cgcccattgt caccgctcta 600  
gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga 660  
agcataccat acctgtgggc aggatgacct atgttctgcc acgcacttg tagccttgga 720  
aaggccactt tgaacctcaa ttttctcaac tgttaaatgg ggtggtaact gctatctcat 780  
aataaagggg aacgtgaaag gaaggcgttt gcatagtgcc tggttgtgca gccaggctgc 840  
agtcaagact agttcccacc aactcgattt taaagccttg caagaagggt gcttgtttgt 900  
cccttgaggg ttcctttgtc gggccaaact ctagaatgcc tcccccttc tttctcattg 960

## crt sequences.ST25

aagagcagac ccaagtccgg gtaacaagga aggggtttcag ggtcctgccc ataaaagggtt	1020
tttcccggcc gccctcagca ccgccccgcc ccgacccccg cagcatctcc aaagcatgca	1080
gagaatgtct ccggctgccc ccgacagact gctccaactt ggtgtctttc cccaaatatg	1140
gagcctgtgt ggagtgagtg gggcgccccg ggggtggtgag ccaagcagac ttccatgggc	1200
agggagggggc gccagcggac ggcagagggg tgacatcact gcctaggcgg cctttaaacc	1260
cctcaccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggaattc	1318
atg ctg ctc cct gtg ccg ctg ctg ctc ggc ctg ctc ggc ctg gcc gcc Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala 1 5 10 15	1366
gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly 20 25 30	1414
tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys 35 40 45	1462
ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys 50 55 60	1510
ggg ctg cag acc agc cag gac gcc cgc ttc tac ggc ctg tcg gcc cga Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg 65 70 75 80	1558
ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala 85 90 95	1606
agg acg ccc gct tct acg ccc tgt cgg ccc gat tcg agc cgt tca gca Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala 100 105 110	1654
aca agg gcc agc cac tgg tgg tgc agt tca ccg tga aac acg agc aga Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro Asn Thr Ser Arg 115 120 125	1702
aca ttg act gcg ggg gcg gct acg tga agc tgt ttc cgg ccg gcc tgg Thr Leu Thr Ala Gly Ala Ala Thr Ser Cys Phe Arg Pro Ala Trp 130 135 140	1750
acc aga agg aca tgc acg ggg act ctg agt aca aca tca tgt ttg gtc Thr Arg Arg Thr Cys Thr Gly Thr Leu Ser Thr Thr Ser Cys Leu Val 145 150 155	1798
ctg aca tct gtg gcc ccg gca cca aga agg ttc acg tca tct tca act Leu Thr Ser Val Ala Pro Ala Pro Arg Arg Phe Thr Ser Ser Ser Thr 160 165 170	1846
aca agg gca aga acg tgc tga tca aca agg aca tcc gtt gca agg acg Thr Arg Ala Arg Thr Cys Ser Ser Thr Arg Thr Ser Val Ala Arg Thr 175 180 185	1894
acg agt tca cac acc tgt aca cgc tga tcg tgc ggc cgg aca aca cgt Thr Ser Ser His Thr Cys Thr Arg Ser Ser Cys Gly Arg Thr Thr Arg 190 195	1942

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190											200					
atg Met 205	agg Arg	tga Arg	aga Leu	ttg Thr	aca Thr 210	aca Thr	gcc Ala	agg Arg	tgg Trp	agt Ser	cgg Arg 215	gct Ala	ccc Pro	tgg Trp	agg Arg	1990
atg Met 220	act Thr	ggg Gly	act Thr	tcc Ser	tac Tyr 225	ccc Pro	cca Pro	aga Arg	aga Arg	taa	agg Arg 230	acc Thr	cag Gln	atg Met	cct Pro	2038
cga Arg 235	agc Ser	ctg Leu	aag Lys	act Thr	ggg Gly 240	acg Thr	agc Ser	ggg Gly	cca Pro	aga Arg 245	tcg Ser	acg Thr	acc Thr	cca Pro	cgg Arg 250	2086
act Thr	cca Pro	agc Ser	ccg Pro	agg Arg 255	act Thr	ggg Gly	aca Thr	agc Ser	ccg Pro 260	agc Ser	aca Thr	tcc Ser	ccg Pro	acc Thr 265	cgg Arg	2134
acg Thr	cga Arg	aga Arg	agc Ser 270	ccg Pro	aag Lys	act Thr	ggg Gly	acg Thr 275	aag Lys	aaa Lys	tgg Trp	acg Thr	gag Glu 280	agt Ser	ggg Gly	2182
agc Ser	cgc Arg	cgg Arg 285	tga Phe	ttc Arg	aga Arg	acc Thr	ccg Pro	agt Ser 290	aca Thr	agg Arg	gtg Val	agt Ser	gga Gly 295	agc Ser	cgc Arg	2230
ggc Gly	aga Arg	tcg Ser 300	aca Thr	acc Thr	ccg Pro	att Ile	aca Thr 305	aag Lys	gca Ala	cct Pro	gga Gly	tcc Ser 310	acc Thr	ccg Pro	aaa Lys	2278
tcg Ser 315	aca Thr	acc Pro	ccg Pro	agt Ser	act Thr	cgc Arg 320	ccg Pro	acg Thr	cta Leu	aca Thr	tct Ser 325	atg Met	cct Pro	acg Thr	aca Thr	2326
gct Ala 330	ttg Leu	ccg Pro	tgc Cys	tgg Trp	gct Ala 335	tgg Trp	acc Thr	tct Ser	ggc Gly	agg Arg 340	tca Ser	agt Ser	cgg Arg	gca Ala	cca Pro 345	2374
tct Ser	tcg Ser	aca Thr	act Thr	tcc Ser 350	tca Ser	tca Ser	cca Pro	acg Thr	atg Met 355	agg Arg	cgt Arg	acg Thr	cag Gln	agg Arg 360	agt Ser	2422
ttg Leu	gca Ala	acg Thr	aga Arg 365	cgt Arg	ggg Gly	gcg Ala	tca Ser	cca Pro 370	aga Arg	cgg Arg	ccg Pro	aga Arg	agc Ser 375	aga Arg	tga	2470
aag Lys	aca Thr	agc Ser	agg Arg 380	acg Thr	agg Arg	agc Ser	agc Ser	gga Gly 385	tga Arg	agg Arg	agg Arg	agg Arg	agg Arg	agg Arg 390	aga Arg	2518
aga Arg	agc Ser	gga Gly	agg Arg 395	agg Arg	agg Arg	agg Arg	agg Arg	ccg Pro 400	agg Arg	agg Arg	acg Thr	agg Arg	agg Arg 405	aca Thr	agg Arg	2566
acg Thr	aca Thr	agg Arg 410	agg Arg	acg Thr	agg Arg	atg Met 415	agg Arg	acg Thr	agg Arg	agg Arg	aca Thr	agg Arg 420	acg Thr	agg Arg	agg Arg	2614
agg Arg 425	agg Arg	agg Arg	cgg Arg	ccg Pro	ccg Pro	gcc Ala 430	agg Arg	cca Pro	agg Arg	acg Thr	agc Ser 435	tgt Cys	ag			2655

crt sequences.ST25

<210> 2  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 2

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
 1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
 20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
 35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
 50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
 65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala  
 85 90 95

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala  
 100 105 110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro  
 115 120

<210> 3  
 <211> 12  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 3

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr  
 1 5 10

<210> 4  
 <211> 45  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

crt sequences.ST25

<400> 4

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu  
1 5 10 15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg  
20 25 30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys  
35 40 45

<210> 5

<211> 17

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 5

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr  
1 5 10 15

Arg

<210> 6

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 6

Ser Cys Gly Arg Thr Thr Arg Met Arg  
1 5

<210> 7

<211> 23

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 7

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly  
1 5 10 15

Thr Ser Tyr Pro Pro Arg Arg  
20

# crt sequences.ST25

<210> 8  
 <211> 56  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 8

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg  
 1 5 10 15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser  
 20 25 30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys  
 35 40 45

Trp Thr Glu Ser Gly Ser Arg Arg  
 50 55

<210> 9  
 <211> 91  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 9

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr  
 1 5 10 15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro  
 20 25 30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys  
 35 40 45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr  
 50 55 60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg  
 65 70 75 80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg  
 85 90

<210> 10

# crt sequences.ST25

<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 10

Lys Thr Ser Arg Thr Arg Ser Ser Gly  
1 5

<210> 11  
<211> 51  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 11

Arg Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg  
1 5 10 15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg  
20 25 30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Arg Pro Arg  
35 40 45

Thr Ser Cys  
50

<210> 12  
<211> 2691  
<212> DNA  
<213> Artificial

<220>  
<223> construct of SM22a promoter and CRT cDNA with HA tag inserted  
into CRT cDNA

<220>  
<221> CDS  
<222> (1319)..(2689)

<220>  
<221> misc\_feature  
<222> (2635)..(2670)  
<223> HA insertion

<400> 12  
ccccttcctt cagatgccac aaggaggtgc tggagttcta tgcaccaata gcttaaacca 60  
gccaggctgg ctgtagtgga ttgagcgtct gaggctgcac ctctctggcc tgcagccagt 120

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tcctgggtga gactgaccct gcctgagggg tctctccttc cctctctcta ctcctttcct	180
ccctctccct ctccctctct ctgtttcctg aggtttccag gattggggat gggactcaga	240
gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca	300
cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac	360
tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg	420
tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggt	480
aggatctttc acgataagga ctattttgaa gggagggagg gtgacactgt cctagtcctc	540
ttaccctagt gtcctccagc cttgccaggc cttaaaccatc cgcccattgt caccgctcta	600
gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga	660
agcataccat acctgtgggc aggatgaccc atgttctgcc acgcacttgg tagccttgga	720
aaggccactt tgaacctcaa ttttctcaac tgttaaatgg ggtggtaact gctatctcat	780
aataaagggg aacgtgaaag gaaggcgttt gcatagtgcc tggttgtgca gccaggctgc	840
agtcaagact agttcccacc aactcgattt taaagccttg caagaagggtg gcttgtttgt	900
cccttgacagg ttcctttgtc gggccaaact ctagaatgcc tccccctttc tttctcattg	960
aagagcagac ccaagtccgg gtaacaagga agggtttcag ggtcctgccc ataaaagggtt	1020
tttcccggcc gccctcagca ccgccccgcc ccgacccccg cagcatctcc aaagcatgca	1080
gagaatgtct ccggctgccc ccgacagact gctccaactt ggtgtctttc cccaaatatg	1140
gagcctgtgt ggagtgagtg gggcgccccg ggggtggtgag ccaagcagac ttccatgggc	1200
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cctcacccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggaattc	1318
atg ctg ctc cct gtg ccg ctg ctg ctc ggc ctg ctc ggc ctg gcc gcc Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala 1 5 10 15	1366
gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly 20 25 30	1414
tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys 35 40 45	1462
ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys 50 55 60	1510
ggg ctg cag acc agc cag gac gcc cgc ttc tac gcc ctg tcg gcc cga Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg 65 70 75 80	1558
ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala 85 90 95	1606



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agg Arg	acg Thr	ccc Pro	gct Ala 100	tct Ser	acg Thr	ccc Pro	tgt Cys 105	cgg Arg	ccc Pro	gat Asp	tcg Ser	agc Ser	cgt Arg 110	tca Ser	gca Ala	1654
aca Thr	agg Arg	gcc Ala 115	agc Ser	cac His	tgg Trp	tgg Trp	tgc Cys 120	agt Ser	tca Ser	ccg Pro	tga	aac Asn	acg Thr 125	agc Ser	aga Arg	1702
aca Thr	ttg Leu	act Thr 130	gcg Ala	ggg Gly	gcg Ala	gct Ala	acg Thr 135	tga	agc Ser	tgt Cys	ttc Phe	cgg Arg	ccg Pro 140	gcc Ala	tgg Trp	1750
acc Thr	aga Arg	agg Arg 145	aca Thr	tgc Cys	acg Thr	ggg Gly	act Thr 150	ctg Leu	agt Ser	aca Thr	aca Thr	tca Ser 155	tgt Cys	ttg Leu	gtc Val	1798
ctg Leu 160	aca Thr 160	tct Ser	gtg Val	gcc Ala	ccg Pro	gca Ala 165	cca Pro	aga Arg	agg Arg	ttc Phe	acg Thr 170	tca Ser	tct Ser	tca Ser	act Thr	1846
aca Thr 175	agg Arg	gca Ala	aga Arg	acg Thr	tgc Cys 180	tga	tca Ser	aca Thr	agg Arg	aca Thr	tcc Ser 185	gtt Val	gca Ala	agg Arg	acg Thr	1894
acg Thr 190	agt Ser	tca Ser	cac His	acc Thr	tgt Cys 195	aca Thr	cgc Arg	tga	tcg Ser	tgc Cys	ggc Gly 200	cgg Arg	aca Thr	aca Thr	cgt Arg	1942
atg Met 205	agg Arg	tga	aga Arg	ttg Leu	aca Thr	aca Thr 210	gcc Ala	agg Arg	tgg Trp	agt Ser	cgg Arg 215	gct Ala	ccc Pro	tgg Trp	agg Arg	1990
atg Met 220	act Thr	ggg Gly	act Thr	tcc Ser	tac Tyr 225	ccc Pro	cca Pro	aga Arg	aga Arg	taa	agg Arg 230	acc Thr	cag Gln	atg Met	cct Pro	2038
cga Arg 235	agc Ser	ctg Leu	aag Lys	act Thr	ggg Gly 240	acg Thr	agc Ser	ggg Gly	cca Pro	aga Arg 245	tcg Ser	acg Thr	acc Thr	cca Pro	cgg Arg 250	2086
act Thr	cca Pro	agc Ser	ccg Pro	agg Arg 255	act Thr	ggg Gly	aca Thr	agc Ser	ccg Pro 260	agc Ser	aca Thr	tcc Ser	ccg Pro	acc Thr 265	cgg Arg	2134
acg Thr	cga Arg	aga Arg	agc Ser 270	ccg Pro	aag Lys	act Thr	ggg Gly	acg Thr 275	aag Lys	aaa Lys	tgg Trp	acg Thr	gag Glu 280	agt Ser	ggg Gly	2182
agc Ser	cgc Arg	cgg Arg 285	tga	ttc Phe	aga Arg	acc Thr	ccg Pro	agt Ser 290	aca Thr	agg Arg	gtg Val	agt Ser	gga Gly 295	agc Ser	cgc Arg	2230
ggc Gly	aga Arg	tcg Ser 300	aca Thr	acc Thr	ccg Pro	att Ile	aca Thr 305	aag Lys	gca Ala	cct Pro	gga Gly 310	tcc Thr	acc Thr	ccg Pro	aaa Lys	2278
tcg Ser	aca Thr 315	acc Thr	ccg Pro	agt Ser	act Thr	cgc Arg 320	ccg Pro	acg Thr	cta Leu	aca Thr	tct Ser 325	atg Met	cct Pro	acg Thr	aca Thr	2326
gct Ala	ttg Leu	ccg Pro	tgc Cys	tgg Trp	gct Ala	tgg Trp	acc Thr	tct Ser	ggc Gly	agg Arg	tca Ser	agt Ser	cgg Arg	gca Ala	cca Pro	2374

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330		335		340		345										
tct	tcg	aca	act	tcc	tca	tca	cca	acg	atg	agg	cgt	acg	cag	agg	agt	2422
Ser	Ser	Thr	Thr	Ser	Ser	Ser	Pro	Thr	Met	Arg	Arg	Thr	Gln	Arg	Ser	
				350					355					360		
ttg	gca	acg	aga	cgt	ggg	gcg	tca	cca	aga	cgg	ccg	aga	agc	aga	tga	2470
Leu	Ala	Thr	Arg	Arg	Gly	Ala	Ser	Pro	Arg	Arg	Pro	Arg	Ser	Arg		
			365					370					375			
aag	aca	agc	agg	acg	agg	agc	agc	gga	tga	agg	agg	agg	agg	agg	aga	2518
Lys	Thr	Ser	Arg	Thr	Arg	Ser	Ser	Gly		Arg	Arg	Arg	Arg	Arg	Arg	
			380					385						390		
aga	agc	gga	agg	agg	agg	agg	agg	ccg	agg	agg	acg	agg	agg	aca	agg	2566
Arg	Ser	Gly	Arg	Arg	Arg	Arg	Arg	Pro	Arg	Arg	Thr	Arg	Arg	Thr	Arg	
			395					400					405			
acg	aca	agg	agg	acg	agg	atg	agg	acg	agg	agg	aca	agg	acg	agg	agg	2614
Thr	Thr	Arg	Arg	Thr	Arg	Met	Arg	Thr	Arg	Arg	Thr	Arg	Thr	Arg	Arg	
			410				415					420				
agg	agg	agg	cgg	ccg	ccg	gcc	tcg	agt	acc	cat	atg	atg	ttc	ctg	act	2662
Arg	Arg	Arg	Arg	Pro	Pro	Ala	Ser	Ser	Thr	His	Met	Met	Phe	Leu	Thr	
			425			430					435					
atg	cta	gac	agg	cca	agg	acg	agc	tgt	ag							2691
Met	Leu	Asp	Arg	Pro	Arg	Thr	Ser	Cys								
440					445											

<210> 13  
 <211> 123  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 13

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
 1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
 20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
 35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
 50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
 65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala  
 85 90 95

crt sequences.ST25

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala  
100 105 110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro  
115 120

<210> 14  
<211> 12  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 14

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr  
1 5 10

<210> 15  
<211> 45  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 15

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu  
1 5 10 15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg  
20 25 30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys  
35 40 45

<210> 16  
<211> 17  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 16

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr  
1 5 10 15

Arg

crt sequences.ST25

<210> 17  
 <211> 9  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 17

Ser Cys Gly Arg Thr Thr Arg Met Arg  
 1 5

<210> 18  
 <211> 23  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 18

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly  
 1 5 10 15

Thr Ser Tyr Pro Pro Arg Arg  
 20

<210> 19  
 <211> 56  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 19

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg  
 1 5 10 15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser  
 20 25 30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys  
 35 40 45

Trp Thr Glu Ser Gly Ser Arg Arg  
 50 55

<210> 20  
 <211> 91  
 <212> PRT  
 <213> Artificial

# crt sequences.ST25

<220>

<223> Synthetic Construct

<400> 20

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr  
1 5 10 15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro  
20 25 30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys  
35 40 45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr  
50 55 60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg  
65 70 75 80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg  
85 90

<210> 21

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 21

Lys Thr Ser Arg Thr Arg Ser Ser Gly  
1 5

<210> 22

<211> 63

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 22

Arg Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg  
1 5 10 15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg  
20 25 30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Ser Ser Thr  
Page 13

# crt sequences.ST25

35

40

45

His Met Met Phe Leu Thr Met Leu Asp Arg Pro Arg Thr Ser Cys  
50 55 60

<210> 23  
<211> 418  
<212> PRT  
<213> Artificial

<220>  
<223> CRT peptide sequence from CRT cDNA

<400> 23

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr  
85 90 95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu  
100 105 110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr  
115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val  
130 135 140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp  
145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val  
165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu  
180 185 190

crt sequences.ST25

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile  
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys  
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu  
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu  
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys  
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr  
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn  
290 295 300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln  
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu  
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr  
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys  
355 360 365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu  
370 375 380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu  
385 390 395 400

Asp Lys Asp Glu Glu Glu Glu Glu Ala Ala Ala Gly Gln Ala Lys Asp  
405 410 415

Glu Leu

crt sequences.ST25

<211> 430  
 <212> PRT  
 <213> Artificial

<220>  
 <223> CRT peptide sequence with HA tag inserted into peptide

<220>  
 <221> MISC\_FEATURE  
 <222> (413)..(424)  
 <223> HA Tag

<400> 24

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala  
 1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly  
 20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys  
 35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys  
 50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg  
 65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr  
 85 90 95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu  
 100 105 110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr  
 115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val  
 130 135 140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp  
 145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val  
 165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu  
 180 185 190



crt sequences.ST25

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile  
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys  
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu  
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu  
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys  
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr  
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn  
290 295 300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln  
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu  
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr  
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys  
355 360 365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu  
370 375 380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu  
385 390 395 400

Asp Lys Asp Glu Glu Glu Glu Glu Ala Ala Ala Gly Leu Glu Tyr Pro  
405 410 415

Tyr Asp Val Pro Asp Tyr Ala Arg Gln Ala Lys Asp Glu Leu  
420 425 430